

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 21, 2002, 08:24:58 ; Search time 76.45 Seconds
(without alignments)
190.079 Million cell updates/sec

Title: US-09-351-778a-12
Perfect score: 84
Sequence: 1 MTCSTIAPTDTYRNTATG.....NEKIHRLDGLKPCSLLOYD 84

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 segs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	66.7	101	12	091236 human adeno
2	56	66.7	101	12	091023 human adeno
3	13	15.5	94	12	012392 human adeno
4	8	9.5	816	15	0994h2 human immun
5	7	8.3	83	12	088422 spliroplasma
6	7	8.3	85	11	09wv20 ratius norv
7	7	8.3	87	10	094h62 oryza sativ
8	7	8.3	160	16	0982G8 rhizobium m
9	7	8.3	160	16	092XL7 rhizobium l
10	7	8.3	197	16	09JSG7 chlamydia p
11	7	8.3	222	1	09JUN5 methanother
12	7	8.3	228	2	09RAX8 oryza pseudomonas
13	7	8.3	245	8	09T319 neptroselm
14	7	8.3	266	16	09PK14 chlamydia m
15	7	8.3	316	10	09C926 arabidopsis
16	7	8.3	387	16	099X15 staphylococ

17	7	8.3	391	16	097GC3	097gc3 clostridium
18	7	8.3	392	10	09AX94	09ax94 oryza sativ
19	7	8.3	404	5	09VIM7	09vim7 drosophila
20	7	8.3	459	16	09A527	09a527 caulobacter
21	7	8.3	490	10	09PSS8	09pss8 oryza sativ
22	7	8.3	495	16	025214	025214 helicobacte
23	7	8.3	495	16	09ZM05	09zm05 helicobacte
24	7	8.3	536	5	043994	043994 caenorhabdi
25	7	8.3	604	5	09VQ31	09vq31 drosophila
26	7	8.3	635	5	09VJ77	09vj77 drosophila
27	7	8.3	649	5	09NKD0	09nk00 drosophila
28	7	8.3	891	2	09RND1	09rkd1 streptomyce
29	7	8.3	1000	15	09MPS5	09mfs6 human immun
30	7	8.3	1000	15	09MPS9	09mfs6 human immun
31	7	8.3	1175	16	09I356	09i356 pseudomonas
32	7	8.3	1427	15	09MP62	09mp62 human immun
33	7	8.3	1427	15	09ST78	09st78 human immun
34	7	8.3	2689	5	09ST78	09st78 human immun
35	6	7.1	26	4	09BUB3	09bub3 homo sapien
36	6	7.1	53	13	09YH36	09yh36 colurnix co
37	6	7.1	64	2	09F347	09f347 streptomyce
38	6	7.1	69	13	09DEC6	09dec6 gallus galli
39	6	7.1	73	15	087603	087603 chimpanzee
40	6	7.1	75	4	09FEN4	09fen4 homo sapien
41	6	7.1	77	12	064888	064888 avian adeno
42	6	7.1	82	16	09PEC9	09pec9 xylella tas
43	6	7.1	83	16	09PEU4	09peu4 xylella tas
44	6	7.1	86	16	092PW6	092pw6 rhizobium m
45	6	7.1	89	10	094J51	094j51 oryza sativ
	6	7.1	89	16	09AA87	09a87 caulobacter

ALIGNMENTS

RESULT 1
ID 091236 PRELIMINARY: PRT: 101 AA.
AC 091236;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 11.6K PROTEIN.
OS Human adenovirus type 2.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PREI;
RA Borchering F., Pring-Akerblom P.;
RT "Adenoviruses of subgenus C with different organ tropism";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ293913; CAC67704.1;
SQ SEQUENCE 101 AA; 11704 MW; E13857DC5691E85B CRC64;

Query Match 66.7%; Score 56; DB 12; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.1e-51;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Caps 0;
OY 29 IALMEVCLIMLILICLRRARRPPIYIVLNPNKIHRLDGLKPCSLLOYD 84
DB 46 IALMEVCLIMLILICLRRARRPPIYIVLNPNKIHRLDGLKPCSLLOYD 101
RESULT 2
ID 091023 PRELIMINARY: PRT: 101 AA.
AC 091023;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 11.6K PROTEIN.
OS Human adenovirus type 2.

CC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=10515;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=105;
 RA Roderburg C.M., Li Y., Trask S.A., Chen Y., Decker J., Robertson D.L.,
 RT "Adenoviruses of subgenus C with different organ tropism."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ293915; CAC67721.1;
 SO SEQUENCE 101 AA; 11662 MW; 914F50AC2F8B284F CRC64;

Query Match 66.7%; Score 56; DB 12; Length 101;
 Best Local Similarity 100.0%; Pred. No. 3, 1e-51;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 IALMFVCLIMMLICLRRARRPRIPVILNPHNEKIHRLDGLKPSLLLOYD 84
 Db 46 IALMFVCLIMMLICLRRARRPRIPVILNPHNEKIHRLDGLKPSLLLOYD 101

RESULT 3
 ID 012392 PRELIMINARY; PRT; 94 AA.
 AC 012392;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-JAN-1998 (TREMBLrel. 05, Last annotation update)
 DE 11.6K PROTEIN.
 GN ADI/E3-11.6K.
 OS Human adenovirus type 1.
 CC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=10513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HANNOVER / ADRIAN;
 RC Reichmann H., Schaefer-Schmidt E., Gelsler B., Hausmann J., Ortman D.,
 RA Bauer U., Flunker G., Seidel W.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y11257; CAA72127.1;
 DR EMBL: Y11032; CAA71916.1;
 SO SEQUENCE 94 AA; 10674 MW; D1148B5AF7171862 CRC64;

Query Match 15.5%; Score 13; DB 12; Length 94;
 Best Local Similarity 100.0%; Pred. No. 5, 7e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 IALMFVCLIMML 41
 Db 40 IALMFVCLIMML 52

RESULT 4
 ID 0994H2 PRELIMINARY; PRT; 816 AA.
 AC 0994H2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TRUNCATED POLYPROTEIN (FRAGMENT).
 GN POL.
 OS Human immunodeficiency virus type 1.
 CC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=98T2013;
 RX MEDLINE=21094715; PubMed=11177395;
 RA Roderburg C.M., Li Y., Trask S.A., Chen Y., Decker J., Robertson D.L.,
 RA Kalish M.L., Shaw G.M., Allen S., Hahn B.H., Gao F.,
 RT "Near full-length clones and reference sequences for subtype C
 isolates for HIV type 1 from three different continents."

RL AIDS Res. Hum. Retroviruses 17:161-168(2001).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=98T2013;
 RA Roderburg C.M., Li Y., Trask S.A., Chen Y., Decker J., Robertson D.L.,
 RA Allen S., Shaw G.M., Hahn B.H., Gao F.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2. ALSO
 CC KNOWN AS THE RETROPEPSIN FAMILY.
 DR EMBL: AF286234; AAK31054.1;
 DR HSSP: P03366; IRLV.
 DR InterPro: IPR001969; Asp_protease.
 DR InterPro: IPR001995; Asp_prot_retrov.
 DR InterPro: IPR003308; Integrase_zn.
 DR InterPro: IPR002156; RNaseH.
 DR InterPro: IPR001584; Rve.
 DR InterPro: IPR000477; RVTse.
 DR Pfam: PF02022; Integrase_zn; 1.
 DR Pfam: PF00073; rnsase; 1.
 DR Pfam: PF00665; rve; 1.
 DR Pfam: PF00077; rvp; 1.
 DR Pfam: PF00078; rvl; 1.
 DR PROSITE: PS00141; ASP_PROTEASE; 1.
 DR PROSITE: PS0175; ASP_PROT_RETROV; 1.
 KW Aspartyl protease; Hydrolase; Polypeptidn;
 KW RNA-directed DNA polymerase.
 FT NON_TER 1 1
 SO SEQUENCE 816 AA; 92110 MW; 3E11128468F93A20 CRC64;

Query Match 9.5%; Score 8; DB 15; Length 816;
 Best Local Similarity 100.0%; Pred. No. 6, 9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 LNLFOIAL 31
 Db 57 LNLFOIAL 64

RESULT 5
 ID 088422 PRELIMINARY; PRT; 83 AA.
 AC 088422;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SPV1-C74, COMPLETE GENOME.
 OS Spiroplasma virus.
 CC Viruses; unclassified viruses.
 OX NCBI_TaxID=12338;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPV1-C74;
 RA Bebear C.M., Aulio P., Bove J., Renaudin J.;
 RT "Spiroplasma citri virus SPV1. Characterization of viral sequences
 present in the Spiroplasma host chromosome."
 RL Curr. Microbiol. 32:1-7(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPV1-C74;
 RA Renaudin J.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U28974; AAA85015.1;
 SO SEQUENCE 83 AA; 9398 MW; D4969373B02BFFA8 CRC64;

Query Match 8.3%; Score 7; DB 12; Length 83;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 TGLTSLAL 24
 Db 30 TGLTSLAL 36

RESULT 6
 ID 09WV20 PRELIMINARY: PRT: 85 AA.
 AC 09WV20;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DE 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE PROTEIN TYROSINE PHOSPHATASE EPSILON (FRAGMENT).
 GN PTPEPSILON.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91115422; PubMed=9114474;
 RA Tanuma N., Nakamura K., Kikuchi K.,
 RT "Distinct promoters control transmembrane and cytosolic protein
 RT tyrosine phosphatase epsilon expression during macrophage
 RT differentiation.";
 RL Eur. J. Biochem. 259:46-54(1999).
 DR EMBL: D89373; BAA78711.1; -.
 FT NON_TER 1 85
 FT 1
 SQ SEQUENCE 85 AA; 9031 MW; CFD2DABE70A02523 CRC64;

Query Match 8.3%; Score 7; DB 11; Length 85;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 PCSLLQ 82
 DB 25 PCSLLQ 31

RESULT 7
 ID 094H62 PRELIMINARY: PRT: 87 AA.
 AC 094H62;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 9.9 KDA PROTEIN.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, NIPPONBARE;
 RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
 RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsalir T.,
 RA Riggs F., Hsiao J., Zismann V., Blunt S., Pal G., Vanaken S.E.,
 RA Usterback T.R., Feldblum T.V., Quackenbush J., Salzberg S.L.,
 RA White O., Fraser C.M.,
 RT "Oryza sativa chromosome 3 BAC OSJNB0057P11 genomic sequence.";
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC084767; AAK72273.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 87 AA; 9941 MW; 092E2A6E9D0A42CE CRC64;

Query Match 8.3%; Score 7; DB 10; Length 87;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 45 LKRRRAR 51
 DB 48 LKRRRAR 54

RESULT 8
 ID 098ZG8 PRELIMINARY: PRT: 160 AA.
 AC 098ZG8;
 DT 01-OCT-2001 (TReMBLrel. 18, Created)
 DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
 DE 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE MR9079 PROTEIN.
 GN MR9079.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFP30309;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneo T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Kouchizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.,
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL: AP003015; BAB54491.1; -.
 KW Plasmid: Complete proteome.
 SQ SEQUENCE 160 AA; 17696 MW; 85A9C5A9233D9A50 CRC64;

Query Match 8.3%; Score 7; DB 16; Length 160;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TGSTIAP 8
 DB 28 TGSTIAP 34

RESULT 9
 ID 092XL7 PRELIMINARY: PRT: 160 AA.
 AC 092XL7;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL PROTEIN SMA2279.
 GN SMA2279.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396509; PubMed=11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barilay-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Gajjal M., Hong A., Huizar L., Hymen R.W., Kahn D., Kahn M.L.,
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Vek K.-C., Davis R.W., Federpsiel N.A., Long S.R.,
 RT "Nucleotide sequence and predicted functions of the entire
 RT Sinorhizobium meliloti pSyma megaplasmid.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 DR EMBL: AB007307; AAK55885.1; -.
 KW Hypothetical protein; Plasmid; Complete proteome.
 SQ SEQUENCE 160 AA; 17966 MW; 9BAB4EBE18A1BE34 CRC64;

Query Match 8.3%; Score 7; DB 16; Length 160;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 2 TGSTAP 8
 |||||
 DB 28 TGSTAP 34

RESULT 10

O9JSG7 PRELIMINARY; PRT; 197 AA.
 AC O9JSG7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE C1142 HYPOTHEICAL PROTEIN_2.
 GN CPJ0259;
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_Taxid=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RA MEDLINE=20330349; PubMed-10871362;
 RA Shiba T., Hiraoka H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CML029 from USA."
 RL Nucleic Acids Res. 28:2311-2314 (2000).
 DR EMBL: AP002545; BAA98469.1; -;
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR InterPro: IPR000511; TonB_boxC.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN.1.
 DR PROSITE: PS00450; TONB_DEPENDENT_REC_1; UNKNOWN.1.
 DR SEQUENCE 197 AA; 22016 MW; EAA69A27851F790D CRC64;

Query Match 8.3%; Score 7; DB 16; Length 197;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ATGLTSA 23
 |||||
 DB 74 ATGLTSA 80

RESULT 11

O9JUN5 PRELIMINARY; PRT; 222 AA.
 AC O9JUN5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1).
 GN TPI.
 OS Methanothermobacter ferrireducens.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanothermobacteraceae;
 OC Methanothermobacter.
 OX NCBI_Taxid=2180;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=V24S;
 RA Schramm A.;
 RA Thesis (1998), Ph.D. thesis, Universitaet-GH Essen, Germany.
 DR EMBL: AJ012065; CAB66160.1; -;
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR000652; Triosephosphate_isomerase.
 DR PRODOM: PD001005; Triosephosphate_isomerase; 1.
 KW Isomerase.
 DR SEQUENCE 222 AA; 23598 MW; 0D9E5F901CB07BA2 CRC64;

Query Match 8.3%; Score 7; DB 1; Length 222;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Caps 0;

OY 56 RPIVLN 62
 |||||
 DB 3 RPIVLN 9

RESULT 12

O9RBX8 PRELIMINARY; PRT; 228 AA.
 AC O9RBX8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HYPOTHEICAL 24.1 KDA PROTEIN.
 OS Pseudomonas indologfera.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Vogesella.
 OX NCBI_Taxid=45465;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC19706;
 RA van de Loo F.J., Keese P., Llewellyn D.;
 RT "Structural and regulatory genes controlling indigoldine production in
 RT Vogesella indologfera: involvement of a peptide synthetase homolog.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TETR/ACNR FAMILY OF TRANSCRIPTIONAL
 CC REGULATORS.
 DR EMBL: AF088856; AAD54003.1; -;
 DR InterPro: IPR001647; HTH_Tetr.
 DR Pfam: PF00440; tetr; 1.
 DR PRINTS: PR00455; HTHTR.
 KW DNA-binding; Hypothetical protein; Transcription regulation.
 DR SEQUENCE 228 AA; 24140 MW; A928DE14F040869B CRC64;

Query Match 8.3%; Score 7; DB 2; Length 228;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 47 RRRARP 53
 |||||
 DB 23 RRRARP 29

RESULT 13

O9T3Y9 PRELIMINARY; PRT; 245 AA.
 AC O9T3Y9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE HYPOTHEICAL 27.2 KDA PROTEIN.
 OS Nephroselmis olivacea.
 OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
 OC Chlorodendraceae; Chlorodendraceae; Nephroselmis.
 OX NCBI_Taxid=31312;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99398694; PubMed-10468994;
 RA Turmel M., Orlis C., Lemieux C.;
 RT "The complete chloroplast DNA sequence of the green alga Nephroselmis
 RT olivacea: Insights into the architecture of ancestral chloroplast
 RT genomes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Turmel M., Orlis C., Lemieux C.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF137379; AAD54918.1; -;
 DR EMBL: AF137379; AAD54871.1; -;

KW Hypothetical protein: Chloroplast.
 SQ SEQUENCE 245 AA; 27217 MW; 74FDF5FD5F229FF7 CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 TGLTSL 24
 Db 204 TGLTSL 210

RESULT 14
 O9PK14 PRELIMINARY; PRT; 266 AA.

AC O9PK14:
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE HYDROLASE, METAL-DEPENDENT, PUTATIVE.
 GN TC00659.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOPN / NIGG;
 RA MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brumham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Uterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolony J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT *Genome sequences of Chlamydia trachomatis MOPN and Chlamydia
 RT pneumoniae AR39.;
 RL Nucleic Acids Res. 28:1397-1406(2000).
 DR EMBL; AE002334; AAF3585.1; -;
 DR TIGR; TC00659; -;
 DR InterPro; IPR001279; Beta_Lactam_met.
 DR Pfam; PF00753; Lactamase_B; 1.
 KW Complete proteome.
 SO SEQUENCE 266 AA; 30286 MW; 4F447AA56C3092DA CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 67 KIHRLDG 73
 Db 66 KIHRLDG 74

RESULT 15
 O9C926 PRELIMINARY; PRT; 316 AA.

AC O9C926:
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE HYPOTHEICAL 34.7 KDA PROTEIN (AT360860/F17014_7).
 GN F17014.7.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroside 11; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unseld M.,

RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Deligny M., Boutry M., Givelli L.A., Macho R., Pulgomech P.,
 RA De Simone V., Choisy N., Artiguenave F., Robert C., Broillet P.,
 RA Wincker P., Cattolico L., Weissbach J., Saurin W., Queller F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wurmacher E., Drzonek H., Erle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonetti B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Jursiak G.,
 RA Reichelt J., Scharte M., Schoen O., Bergues M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-Diaro C., Purnelle B., Masny D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
 RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Meyer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Maltz A., Uterback T., Fujil C.Y., Shea T.P.,
 RA Creasy T.H., Haas B., Maltz R., Wu D., Peterson J., Van Aken S.,
 RA Pai G., Miltischer J., Sellers P., Gill J.E., Feldlyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Ideawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
 RT *Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RT thaliana.;
 RL Nature 408:820-822(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
 RA Bower L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Kallin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT *Arabidopsis ORF clones.;
 RN Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 SO [3]

RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
 RA Bower L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
 RA Kallin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K.,
 RA Davis R.W., Theologis A., Ecker J.R.;
 RT *Arabidopsis cDNA clones.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC012562; AAG51364.1; -;
 DR EMBL; AY056087; AAL06975.1; -;
 DR EMBL; AY045678; AAK74036.1; -;
 KW Hypothetical protein.
 SO SEQUENCE 316 AA; 34732 MW; 5B54FCF59A5B5B CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 SALNLPO 28
 Db 146 SALNLPO 152

Search completed: June 21, 2002, 08:24:59
 Job time: 284 sec
